**SUPPORTING INFORMATION**

**Supplementary Figures**

**Fig S1. Read coverage along chromosomes of hybrid isolate 118 identifies putative chromosome aneuploidy.** Mapping of Illumina reads from isolate 118 showed a 1.5 times higher read coverage for chromosome 8 (average raw read coverage = 26.1) relative to the other eleven chromosomes (average raw read coverage: 17.0). Coverage is depicted along each chromosome for 10Kb windows. In spite of this chromosomal abnormality the hybrid isolate 118 does not stand out phenotypically in this study, and the observation was not studied further here.

**Fig S2. Recombination blocks of the F1 hybrid population (Ptt0-1 × PtmFGO).** Chromosomes in the genome of Ptt0-1 are shown on the x-axis and isolate number is shown on the y-axis. Red blocks indicate the isolate inherited alleles from Ptt0-1 and blue blocks indicate the isolate inherited alleles from PtmFGO. Purple blocks are alleles of undetermined parentage.

**Fig S3. Neighbornet graph of 166 *P. teres* isolates.** *P. teres* f. *teres* isolates are labeled with red nodes and *P. teres* f. *maculata* isolates are labeled in blue.

**Fig S4. Field isolates of *Ptt* and *Ptm* exhibit genetic differentiation along genomes.** Nucleotide diversity, and divergence of the *P. teres* f. *teres* (*Ptt*) and *P. teres* f. *maculata* (*Ptm*) population from Iran. Chromosomes and positions are represented on the x-axis along with gene density (gray segments), effectors (green), and biosynthetic gene clusters (blue). Level of diversity and divergence are shown on the y-axis. The top panels are the nucleotide diversity (π) of *Ptt* and *Ptm*, and the bottom panels are divergence between lineages (Dxy and Fst). Dashed lines indicated the top 10% values for each statistic. Black arrows at chromosome 3: positions 2613142 - 2655000, chromosome 6: positions 1503851 - 1504863, and chromosome 8: positions 549752 - 550000 indicate regions showing high Dxy, Fst, and linkage disequilibrium and overlap with virulence QTLs.

**Supplementary Tables**

**Table S1.** Coordinates of Biosynthetic Gene Clusters (BGCs) and effectors in the Ptt0-1 and FGOB10Ptm-1 genomes.

**Table S2.** Sequencing statistics of the Ptt0-1 × Ptt15A F1 haploid progeny.

**Table S3.** Sequencing statistics of the PtmFGO × PtmSG1 F1 haploid progeny.

**Table S4.** List hybrid haploid progeny from the Ptt0-1 × PtmFGO crossing experiments and sequencing statistics.

**Table S5.** Average read coverage of Illumina sequencing for hybrid population

**Table S6.** Recombination hotspots in Ptt0-1 × Ptt15A, PtmFGO × PtmSG1, and Ptt0-1 × PtmFGO crosses.Coordinates for the recombination hotspots are shown for each chromosome and within a 10kb region.

**Table S7.** Isolates used in population analyses with corresponding information on subspecies, location of origin and sequencing information.

**Table S8.** Coordinates of Dxy and Fst outliers, and associated putative DMIs.

**Supplementary File 1.** Interchromosomal odds ratio across the Ptt0-1 genome. The statistic is calculated by multiplying the number of the Ptt0-1 and PtmFGO parental genotypes and dividing by the product of the hybrid genotypes. Hybrid genotypes were identified as one allele at one locus coming from Ptt0-1 and the other allele at another locus came from PtmFGO. Parental genotypes were identified as having both alleles from Ptt0-1 or both alleles from PtmFGO. Values greater than 1 indicate higher parental genotype frequency, less than 1 indicates higher hybrid frequency, and equal to 1 indicate parental and hybrid frequencies are equal (Greig et al. 2002).